

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/746,361DATE: 02/26/97
TIME: 14:40:23

INPUT SET: S15763.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: ANDERSON, Darrell R.
6 HANNA, Nabil
7 BRAMS, Peter
8
9 (ii) TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING
10 INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND THE HUMAN B7.1
11 AND B7.2 CO-STIMULATORY ANTIGENS
12
13 (iii) NUMBER OF SEQUENCES: 6
14
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
17 (B) STREET: P.O. Box 1404
18 (C) CITY: Alexandria
19 (D) STATE: Virginia
20 (E) COUNTRY: United States
21 (F) ZIP: 22313-1404
22
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28
29 (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER: US 08/746,361
31 (B) FILING DATE: 08-NOV-1996
32 (C) CLASSIFICATION:
33
34 (vii) PRIOR APPLICATION DATA:
35 (A) APPLICATION NUMBER: US 08/487,550
36 (B) FILING DATE: 07-JUN-1995
37
38 (viii) ATTORNEY/AGENT INFORMATION:
39 (A) NAME: Teskin, Robin L.
40 (B) REGISTRATION NUMBER: 35,030
41 (C) REFERENCE/DOCKET NUMBER: 012712-256
42
43 (ix) TELECOMMUNICATION INFORMATION:
44 (A) TELEPHONE: (703) 836-6620
45 (B) TELEFAX: (703) 836-2021
46

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48 (2) INFORMATION FOR SEQ ID NO:1:

49

50 (i) SEQUENCE CHARACTERISTICS:

51 (A) LENGTH: 705 base pairs

52 (B) TYPE: nucleic acid

53 (C) STRANDEDNESS: single

54 (D) TOPOLOGY: linear

55

56 (ii) MOLECULE TYPE: DNA (genomic)

57

58 (ix) FEATURE:

59 (A) NAME/KEY: CDS

60 (B) LOCATION: 1..705

61

62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

63

64 ATG AGG GTC CCC GCT CAG CTC CTG GGG CTC CTG CTG CTC TGG CTC CCA 48

65 Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro

66 1 5 10 15

67

68 GGT GCA CGA TGT GCC TAT GAA CTG ACT CAG CCA CCC TCG GTG TCA GTG 96

69 Gly Ala Arg Cys Ala Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val

70 20 25 30

71

72 TCC CCA GGA CAG ACG GCC AGG ATC ACC TGT GGG GGA GAC AAC AGT AGA 144

73 Ser Pro Gly Gln Thr Ala Arg Ile Thr Cys Gly Gly Asp Asn Ser Arg

74 35 40 45

75

76 AAT GAA TAT GTC CAC TGG TAC CAG CAG AAG CCA GCG CGG GCC CCT ATA 192

77 Asn Glu Tyr Val His Trp Tyr Gln Gln Lys Pro Ala Arg Ala Pro Ile

78 50 55 60

79

80 CTG GTC ATC TAT GAT GAT AGT GAC CGG CCC TCA GGG ATC CCT GAG CGA 240

81 Leu Val Ile Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg

82 65 70 75 80

83

84 TTC TCT GGC TCC AAA TCA GGG AAC ACC GCC ACC CTG ACC ATC AAC GGG 288

85 Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Thr Leu Thr Ile Asn Gly

86 85 90 95

87

88 GTC GAG GCC GGG GAT GAG GCT GAC TAT TAC TGT CAG GTG TGG GAC AGG 336

89 Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Arg

90 100 105 110

91

92 GCT AGT GAT CAT CCG GTC TTC GGA GGA GGG ACC CGG GTG ACC GTC CTA 384

93 Ala Ser Asp His Pro Val Phe Gly Gly Gly Thr Arg Val Thr Val Leu

94 115 120 125

95

96 GGT CAG CCC AAG GCT GCC CCC TCG GTC ACT CTG TTC CCG CCC TCC TCT 432

97 Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser

98 130 135 140

99

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100	GAG GAG CTT CAA GCC AAC AAG GCC ACA CTG GTG TGT CTC ATA AGT GAC	480
101	Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp	
102	145 150 155 160	
103		
104	TTC TAC CCG GGA GCC GTG ACA GTG GCC TGG AAG GCA GAT AGC AGC CCC	528
105	Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro	
106	165 170 175	
107		
108	GTC AAG GCG GGA GTG GAG ACC ACC ACA CCC TCC AAA CAA AGC AAC AAC	576
109	Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn	
110	180 185 190	
111		
112	AAG TAC GCG GCC AGC AGC TAC CTG AGC CTG ACG CCT GAG CAG TGG AAG	624
113	Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys	
114	195 200 205	
115		
116	TCC CAC AGA AGC TAC AGC TGC CAG GTC ACG CAT GAA GGG AGC ACC GTG	672
117	Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val	
118	210 215 220	
119		
120	GAG AAG ACA GTG GCC CCT ACA GAA TGT TCA TGA	705
121	Glu Lys Thr Val Ala Pro Thr Glu Cys Ser *	
122	225 230 235	
123		
124		

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

141	ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCT CCC AGA TGG	48
142	Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp	
143	240 245 250	
144		
145	GTC CTG TCC GAG GTG AAG CTG CAG CAG TGG GGC GAA GGA CTT CTG CAG	96
146	Val Leu Ser Glu Val Lys Leu Gln Gln Trp Gly Glu Gly Leu Leu Gln	
147	255 260 265	
148		
149	CCT TCG GAG ACC CTG TCC CGC ACC TGC GTT GTC TCT GGT GGC TCC ATC	144
150	Pro Ser Glu Thr Leu Ser Arg Thr Cys Val Val Ser Gly Gly Ser Ile	
151	270 275 280	
152		

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153	AGC	GGT	TAC	TAC	TAC	TGG	ACC	TGG	ATC	CGC	CAG	ACC	CCA	GGG	AGG	GGA	192
154	Ser	Gly	Tyr	Tyr	Tyr	Trp	Thr	Trp	Ile	Arg	Gln	Thr	Pro	Gly	Arg	Gly	
155		285					290					295					
156																	
157	CTG	GAG	TGG	ATT	GGC	CAT	ATT	TAT	GGT	AAT	GGT	GCG	ACC	ACC	AAC	TAC	240
158	Leu	Glu	Trp	Ile	Gly	His	Ile	Tyr	Gly	Asn	Gly	Ala	Thr	Thr	Asn	Tyr	
159	300					305					310					315	
160																	
161	AAT	CCC	TCC	CTC	AAG	AGT	CGA	GTC	ACC	ATT	TCA	AAA	GAC	ACG	TCC	AAG	288
162	Asn	Pro	Ser	Leu	Lys	Ser	Arg	Val	Thr	Ile	Ser	Lys	Asp	Thr	Ser	Lys	
163					320					325					330		
164																	
165	AAC	CAG	TTC	TTC	CTG	AAC	TTG	AAT	TCT	GTG	ACC	GAC	GCG	GAC	ACG	GCC	336
166	Asn	Gln	Phe	Phe	Leu	Asn	Leu	Asn	Ser	Val	Thr	Asp	Ala	Asp	Thr	Ala	
167				335				340				345					
168																	
169	GTC	TAT	TAC	TGT	GCG	AGA	GGC	CCT	CGC	CCT	GAT	TGC	ACA	ACC	ATT	TGT	384
170	Val	Tyr	Tyr	Cys	Ala	Arg	Gly	Pro	Arg	Pro	Asp	Cys	Thr	Thr	Ile	Cys	
171			350				355					360					
172																	
173	TAT	GGC	GGC	TGG	GTC	GAT	GTC	TGG	GGC	CCG	GGA	GAC	CTG	GTC	ACC	GTC	432
174	Tyr	Gly	Gly	Trp	Val	Asp	Val	Trp	Gly	Pro	Gly	Asp	Leu	Val	Thr	Val	
175		365					370					375					
176																	
177	TCC	TCA	GCT	AGC	ACC	AAG	GGC	CCA	TCG	GTC	TTC	CCC	CTG	GCA	CCC	TCC	480
178	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	
179	380					385				390						395	
180																	
181	TCC	AAG	AGC	ACC	TCT	GGG	GGC	ACA	GCG	GCC	CTG	GGC	TGC	CTG	GTC	AAG	528
182	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	
183					400				405					410			
184																	
185	GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTG	TCG	TGG	AAC	TCA	GGC	GCC	CTG	576
186	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	
187				415				420					425				
188																	
189	ACC	AGC	GGC	GTG	CAC	ACC	TTC	CCG	GCT	GTC	CTA	CAG	TCC	TCA	GGA	CTC	624
190	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	
191			430					435					440				
192																	
193	TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	672
194	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	
195		445					450					455					
196																	
197	CAG	ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	720
198	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	
199	460					465				470						475	
200																	
201	GAC	AAG	AAA	GCA	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	768
202	Asp	Lys	Lys	Ala	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	
203					480					485					490		
204																	
205	CCG	TGC	CCA	GCA	CCT	GAA	CTC	CTG	GGG	GGA	CCG	TCA	GTC	TTC	CTC	TTC	816

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206	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	
207				495					500						505		
208																	
209	CCC	CCA	AAA	CCC	AAG	GAC	ACC	CTC	ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	864
210	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	
211			510					515					520				
212																	
213	ACA	TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAC	GAA	GAC	CCT	GAG	GTC	AAG	TTC	912
214	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	
215		525					530				535						
216																	
217	AAC	TGG	TAC	GTG	GAC	GGC	GTG	GAG	GTG	CAT	AAT	GCC	AAG	ACA	AAG	CCG	960
218	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	
219	540					545					550					555	
220																	
221	CGG	GAG	GAG	CAG	TAC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC	GTC	CTC	ACC	1008
222	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	
223				560					565						570		
224																	
225	GTC	CTG	CAC	CAG	GAC	TGG	CTG	AAT	GGC	AAG	GAG	TAC	AAG	TGC	AAG	GTC	1056
226	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	
227				575					580					585			
228																	
229	TCC	AAC	AAA	GCC	CTC	CCA	GCC	CCC	ATC	GAG	AAA	ACC	ATC	TCC	AAA	GCC	1104
230	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	
231			590					595					600				
232																	
233	AAA	GGG	CAG	CCC	CGA	GAA	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CGG	1152
234	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	
235		605					610					615					
236																	
237	GAT	GAG	CTG	ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GGC	1200
238	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	
239	620					625				630						635	
240																	
241	TTC	TAT	CCC	AGC	GAC	ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	CAG	CCG	1248
242	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	
243				640					645						650		
244																	
245	GAG	AAC	AAC	TAC	AAG	ACC	ACG	CCT	CCC	GTG	CTG	GAC	TCC	GAC	GGC	TCC	1296
246	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	
247				655					660					665			
248																	
249	TTC	TTC	CTC	TAC	AGC	AAG	CTC	ACC	GTG	GAC	AAG	AGC	AGG	TGG	CAG	CAG	1344
250	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	
251			670					675					680				
252																	
253	GGG	AAC	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG	GCT	CTG	CAC	AAC	CAC	1392
254	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	
255		685					690					695					
256																	
257	TAC	ACG	CAG	AAG	AGC	CTC	TCC	CTG	TCT	CCG	GGT	AAA	TGA				1431
258	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	*				

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